

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: March 10, 2003, 18:28:11 ; Search time 20004.5 Seconds
(without alignments)
1964.002 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_hgt.*
- 3: gb_in.*
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- 39: em_vl.*
- 40: em_vl.*
- 41: em_vl.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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3	1350	100.0	1941	9	AF262016	AF262016 Homo sapi
4	1350	100.0	3612	9	AY032736	AY032736 Homo sapi
5	1350	100.0	3653	9	AF284095	AF284095 Homo sapi
6	1350	100.0	204908	9	AL158163	AL158163 Human DNA
7	1348.4	99.9	1350	6	AX350513	AX350513 Sequence
8	1348.4	99.9	1353	9	AF316894	AF316894 Homo sapi
9	1327	98.3	3604	9	HUMADRA2R	M23533 Human alpha
10	1319	97.7	1521	9	HUMADRA	M18415 Human plate
11	1150	85.2	1728	4	FIGA2AR	J05652 Porcine alp
12	1133.8	84.0	2291	10	CPU25722	U25722 Cavia porce
13	1106.8	82.0	1552	10	RRU79031	U79031 Rattus norv
14	1095.6	81.2	1380	10	RATR20	M62372 Rat alpha-2
15	1095	81.1	2923	4	BTU79030	U79030 Bos taurus
16	1084.4	80.3	1454	10	MUSALP2ADB	M93377 Mouse alpha
17	1084.4	80.3	204317	2	AC113491	AC113491 Mus muscu
18	917	67.9	7353	6	AX344975	AX344975 Sequence
19	917	67.9	7353	6	AX348496	AX348496 Sequence
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34	462	34.2	1380	10	RATR20	M62371 Rat alpha-2
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36	460.4	34.1	5221	10	MUSADRA	M97516 Mus musculu
37	458.8	34.0	1704	10	RATA2BADR	M58316 Rat alpha-2
38	446	33.0	22842	9	AC092603	AC092603 Homo sapi
39	444.4	32.9	1344	6	AX350490	AX350490 Sequence
40	444.4	32.9	1344	9	AF316895	AF316895 Homo sapi
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44	425	31.5	1149	4	CVI315935	AJ315935 Chaetophr
45	411.8	30.5	1492	4	DVU04310	U04310 Didelphis v

ALIGNMENTS

RESULT 1	AX350512	Sequence 24 from Patent WO0179561.	1350 bp	DNA	linear	PAT 06-FEB-2002
LOCUS	AX350512	Sequence 24 from Patent WO0179561.				
DEFINITION	AX350512					
ACCESSION	AX350512					
VERSION	AX350512.1	GI:18616107				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					

REFERENCE
1
Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 24 23-OCT-2001;





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AUTHORS
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REMARK
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FEATURES
source

AP262016
Homo sapiens adrenergic receptor alpha-2A gene, complete cds.
AP262016
AP262016.2
GI:9864781
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1941)
Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosei,E.
A search for genetic variability in the human alpha-2 adrenergic
receptor on chromosome 10
Unpublished
2 (bases 1 to 1941)
Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosei,E.
Direct Submission
Submitted (29-APR-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
3 (bases 1 to 1941)
Castellano,M., Giacche',M., Rossi,F., Rivadossi,F., Perani,C.,
Beschi,M. and Agabiti Rosei,E.
Direct Submission
Submitted (22-AUG-2000) Medical and Surgical Sciences, University
of Brescia, Spedali Civili di Brescia, Brescia I-25100, Italy
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RESULT 10
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DEFINITION
ACCESSION M18415
VERSION    M18415.1 GI:178191
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SOURCE      Human (lambda-EMBL 3 library) DNA.
ORGANISM    Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Koblika,B.K., Matsui,H., Koblika,T.S., Yang-Feng,T.L., Francke,U.,
            Caron,M.G., Lefkowitz,J. and Regan,J.W.
            Cloning, sequencing, and expression of the gene coding for the
            human platelet alpha 2-adrenergic receptor
            Science 238 (4827), 650-656 (1987)
JOURNAL     88042789
MEDLINE     PUBMED
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:29:07 ; Search time 4002.27 Seconds
(without alignments)
9816.632 Million cell updates/sec

Title: US-09-636-259B-2

Perfect score: 1350

Sequence: 1 atgggtccctgcagccgga.....ggacaggaagcgatcgtg 1350

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1350	100.0	1350	6	AX350513	Sequence
2	1350	100.0	1353	9	AF316894	Homo sapi
3	1348.4	99.9	1350	6	AX350512	Sequence
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7	1348.4	99.9	3653	9	AF284095	Homo sapi
8	1348.4	99.9	204908	9	AL158163	Human DNA
9	1325.4	98.2	3604	9	HUMADRA2R	M23533 Human alpha
10	1317.4	97.6	1521	9	HUMADRA	M18415 Human plate
11	1150	85.2	1728	4	PIC2AR	J05652 Porcine alp
12	1133.8	84.0	2291	10	CFU25722	U25722 Cavia porce
13	1105.2	81.9	1552	10	RRU79031	U79031 Rattus norv
14	1094	81.0	1380	10	RATRG20	M62372 Rat alpha-2
15	1093.4	81.0	2923	4	BTU79030	U79030 Bos taurus
16	1082.8	80.2	1454	10	MUSALP2ADB	M99377 Mouse alpha
17	1082.8	80.2	204317	2	AC113491	AC113491 Mus muscu
18	915.4	67.8	7353	6	AX344975	Sequence
19	915.4	67.8	7353	6	AX348496	Sequence
20	836.4	62.0	7353	6	AX344974	Sequence
21	836.4	62.0	7353	6	AX348495	Sequence
22	528	39.1	1386	6	AX350528	Sequence
23	527.4	39.1	1491	9	HUMADRA2C	J03853 Human kidne
24	527.4	39.1	4850	9	HSU72648	U72648 Homo sapien
25	524.8	38.9	1389	9	AF280399	AF280399 Homo sapi
26	517.8	38.4	1995	10	CPU25724	U25724 Cavia porce
27	517.2	38.3	1374	6	AX350530	Sequence
28	514	38.1	1377	9	AF280400	AF280400 Homo sapi
29	512.4	38.0	1382	6	E07358	E07358 gDNA encodi
30	512.4	38.0	1382	9	HUMA2C1IA	D15338 Human alpha
31	505.2	37.4	3461	5	TRU345040	TRU345040 Takifugu
32	464.4	34.4	1503	10	MUSALP2ADA	M99376 Mouse alpha
33	464.4	34.4	1745	10	RATA2AR	D00819 Rattus norv
34	463.6	34.3	1380	10	RATRG10	M62371 Rat alpha-2
35	462	34.2	2991	10	RNA2C4	X57659 R. norvegic
36	462	34.2	5221	10	MUSADRA	M57516 Mus musculu
37	460.4	34.1	1704	10	RATA2ADR	M58316 Rat alpha-2
38	447.6	33.2	22842	9	AC092603	AC092603 Homo sapi
39	446	33.0	1344	6	AX350490	AX350490 Sequence
40	446	33.0	1344	9	AF316895	AF316895 Homo sapi
41	443	32.8	1353	6	AX350489	AX350489 Sequence
42	443	32.8	9842	9	AF005900	AF005900 Homo sapi
43	439.8	32.6	2072	9	HUMADRA2RA	M34041 Human alpha
44	426.6	31.6	1149	4	CVI315935	AJ315935 Chaetophr
45	413	30.6	1492	4	DV004310	U04310 Didelphis v

ALIGNMENTS

RESULT 1
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Qy	61	GGCGGGCCCCGGGACACCCCTTACTCCCTGCAGGTGACGCTGACGTGTGTGCTCGCC	120
Db	61	GGCGGGCCCCGGGACACCCCTTACTCCCTGCAGGTGACGCTGACGTGTGTGCTCGCC	120
Qy	121	GGCCTGCTCATGCTGCTCAGCCGTGTTCGGCAACGTCGCTCATCATCGCCGTGTTCAGG	180
Db	121	GGCCTGCTCATGCTGCTCAGCCGTGTTCGGCAACGTCGCTCATCATCGCCGTGTTCAGG	180
Qy	181	AGCGGGCGCTCAAGGCGCCCCAAAACCTCTTCTGGTGTCTCTGGCCTCGGCCGACATC	240
Db	181	AGCGGGCGCTCAAGGCGCCCCAAAACCTCTTCTGGTGTCTCTGGCCTCGGCCGACATC	240
Qy	241	CTGGTGGCCACGCTCGTCATCCCTTTCTGCTGGCCCAACGAGTCTAGTGGTACT	300
Db	241	CTGGTGGCCACGCTCGTCATCCCTTTCTGCTGGCCCAACGAGTCTAGTGGTACT	300
Qy	301	TTCCGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGTCTTCTGCACGTCTGCC	360
Db	301	TTCCGCAAGGCTTGGTGGAGATCTACCTGGCGCTCGACGTGTCTTCTGCACGTCTGCC	360
Qy	361	ATCGTGCACCTGTGGCCCATAGCCTGGAACGCTACTTGGTCCATCACAAGGCCATCGAG	420
Db	361	ATCGTGCACCTGTGGCCCATAGCCTGGAACGCTACTTGGTCCATCACAAGGCCATCGAG	420
Qy	421	TACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCGTGTGGGTCACTC	480
Db	421	TACAACCTGAAGCGCACGCGCGCGCATCAAGGCCATCATCATCACCGTGTGGGTCACTC	480
Qy	481	TCGGCGCTCATCTCCTTCCCGCGCTCATCTCCATCTGAGAAGAGGCGCGCGCGCGG	540
Db	481	TCGGCGCTCATCTCCTTCCCGCGCTCATCTCCATCTGAGAAGAGGCGCGCGCGCGG	540
Qy	541	CCGACGCGCGGAGCGCGCTGCGAGATCAAGACCAAGAGTGTGTACGTCACTCTGTCG	600
Db	541	CCGACGCGCGGAGCGCGCTGCGAGATCAAGACCAAGAGTGTGTACGTCACTCTGTCG	600
Qy	601	TGCATGGCTTCCTTCTTCGCTCCCTCGCTCATCTATGATCTCTGCTTACGTGCGCATCTAC	660
Db	601	TGCATGGCTTCCTTCTTCGCTCCCTCGCTCATCTATGATCTCTGCTTACGTGCGCATCTAC	660
Qy	661	CAGATGCCAAGCGTCGACCCGCTGCCACCCAGCCGCGGGGTCCGGACGCCCTCGCC	720
Db	661	CAGATGCCAAGCGTCGACCCGCTGCCACCCAGCCGCGGGGTCCGGACGCCCTCGCC	720
Qy	721	GCGCCCGGGGGGACCCGAGGCGAGGCCCAGAGGTCTTGGCCCCCGAGCGACGCGGGC	780
Db	721	GCGCCCGGGGGGACCCGAGGCGAGGCCCAGAGGTCTTGGCCCCCGAGCGACGCGGGC	780
Qy	781	CCGGGGGGCGCAGGCGCCGACCCGCTGACCCACCGCTTACGCGGCGCCCTTGGGAGCCC	840
Db	781	CCGGGGGGCGCAGGCGCCGACCCGCTTACGCGGCGCCCTTGGGAGCCC	840
Qy	841	CGCGCGCGCGGGCGCGCACCCAGCGCTTGGACCTTGGAGGAGAGCTGCTTCTCCGAC	900
Db	841	CGCGCGCGCGGGCGCGCACCCAGCGCTTGGACCTTGGAGGAGAGCTGCTTCTCCGAC	900
Qy	901	CACGCCGAGCGGCTTCCAGGGCCCCGACCCGAGCGCGGTTCGCCGGGGCAAGGCAAG	960
Db	901	CACGCCGAGCGGCTTCCAGGGCCCCGACCCGAGCGCGGTTCGCCGGGGCAAGGCAAG	960
Qy	961	CGCCGACGAGCCAGGTGAAGCGGGGCGACACCTTCCGCGCGCGGGCGGGGGCGGACG	1020
Db	961	CGCCGACGAGCCAGGTGAAGCGGGGCGACACCTTCCGCGCGCGGGCGGGGGCGGACG	1020
Qy	1021	GGGATCGGGACCGCGCTCGAGGGCGGGGAGGAGCGCTCGGGGCTTGCCAGGGCGTCG	1080
Db	1021	GGGATCGGGACCGCGCTCGAGGGCGGGGAGGAGCGCTCGGGGCTTGCCAGGGCGTCG	1080
Qy	1081	CGCTGGCGGGGGCGGCAGAACCCGAGAGAGCGCTTACGTCTGCTGGCGCGGTGCTATC	1140
Db	1081	CGCTGGCGGGGGCGGCAGAACCCGAGAGAGCGCTTACGTCTGCTGGCGCGGTGCTATC	1140

Qy	1141	GGAGTGTTCGTGGTGTCTGCTGGTTCCCTCTTCTTACCTACAGCTCAGCGCGTGGG	1200
Db	1141	GGAGTGTTCGTGGTGTCTGCTGGTTCCCTCTTCTTACCTACAGCTCAGCGCGTGGG	1200
Qy	1201	TGCTCCGTGGCAGCAGCGCTCTTCAAAATCTTCTTCGTTCGGCTACTGCAACAGCTCG	1260
Db	1201	TGCTCCGTGGCAGCAGCGCTCTTCAAAATCTTCTTCGTTCGGCTACTGCAACAGCTCG	1260
Qy	1261	TTGAACCCGGTTCATCTACACATCTTCAACACAGATTTCCGCGCGCGCTTCAAGAAGATC	1320
Db	1261	TTGAACCCGGTTCATCTACACATCTTCAACACAGATTTCCGCGCGCGCTTCAAGAAGATC	1320
Qy	1321	CTCTGTCTGGGGGACAGGAAGCGGATCGT	1350
Db	1321	CTCTGTCTGGGGGACAGGAAGCGGATCGT	1350

RESULT 4	
LOCUS	AF281308
DEFINITION	Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete cds.
ACCESSION	AF281308
VERSION	AF281308.1
KEYWORDS	GI:9652209
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE	An asn to lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling
JOURNAL	J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE	70556293
PUBMED	10948191
REFERENCE	2 (bases 1 to 1353)
AUTHORS	Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
TITLE	Direct Submission
JOURNAL	Submitted (22-JUN-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267 USA

Db 1081



02

02

02

02



of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PBACE3.6

This sequence is the entire insert of clone RP11-348N5 The true
left end of clone RP11-479A21 is at 179266 in this sequence. The
true right end of clone RP11-313D6 is at 44800 in this sequence.

FEATURES

Location/Qualifiers
1. 204908
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-348N5"
/clone_lib="RP11-11.2"
BASE COUNT 62115 a 36724 c 39536 g 66533 t
ORIGIN

Query Match 99.9%; Score 1348.4; DB 9; Length 204908;
Best Local Similarity 99.9%; Pred. No. 1.5e-159;
Matches 1349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCCCTGACGGGACGGGGGACCGAGCTGGAACGGGACCGAGGGCGGGG 60
Db 195570 ATGGGCTCCCTGACGGGACGGGGGACCGAGCTGGAACGGGACCGAGGGCGGGG 195629

QY 61 GGGGGGCGGGGCGCCACCCCTTACTCCCTGACGCTGACGCTGCTGCTGCTGCTG 120
Db 195630 GGGGGGCGGGGCGCCACCCCTTACTCCCTGACGCTGACGCTGCTGCTGCTG 195689

QY 121 GGCTGTCTATGTCTACCGTGTTCGGCAACGCTGCTGCTATCATCATCGCTTCACG 180
Db 195690 GGCTGTCTATGTCTACCGTGTTCGGCAACGCTGCTGCTATCATCATCGCTTCACG 195749

QY 181 AGCGGCGCTCAAGGGGCGCCAAACCTTCTCTGGTCTCTGCTGCTGCTGCTGCTG 240
Db 195750 AGCGGCGCTCAAGGGGCGCCAAACCTTCTCTGGTCTCTGCTGCTGCTGCTGCTG 195809

QY 241 CTGTTGGCCACGCTGCTATCCCTTCTCTGGTCTCTGCTGCTGCTGCTGCTGCTG 300
Db 195810 CTGTTGGCCACGCTGCTATCCCTTCTCTGGTCTCTGCTGCTGCTGCTGCTGCTG 195869

QY 301 TTGGGCAAGCTTGTGCGAGATCTACCTGGGCTCGAGCTGCTCTTCTGCAAGTCTGCT 360
Db 195870 TTGGGCAAGCTTGTGCGAGATCTACCTGGGCTCGAGCTGCTCTTCTGCAAGTCTGCT 195929

QY 361 ATGCTGACCTGTGGCGCATCAGCTGAGCGCTACTGCTGCTATCATCATCAGGCGCATCGAG 420
Db 195930 ATGCTGACCTGTGGCGCATCAGCTGAGCGCTACTGCTGCTATCATCATCAGGCGCATCGAG 195989

QY 421 TACAACCTGAAGCGCACGGCGCGCCGATCAAGGCCATCATCATCACCCTGTGGGTCTATC 480
Db 195990 TACAACCTGAAGCGCACGGCGCGCCGATCAAGGCCATCATCATCACCCTGTGGGTCTATC 196049

QY 481 TCGGCGGTATCTCTTCCGCGCGCTCATCTCCATCGAGAAGGGCGGGCGGGCGGCG 540
Db 196050 TCGGCGGTATCTCTTCCGCGCGCTCATCTCCATCGAGAAGGGCGGGCGGGCGGCGG 196109

QY 541 CCGCAGCGCGCGGCGGCTGCGAGATCAAGCACGACGAGTGTACCTCATCTCTGCTG 600
Db 196110 CCGCAGCGCGCGGCGGCTGCGAGATCAAGCACGAGTGTACCTCATCTCTGCTGCTG 196169

QY 601 TGCATCGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 196170 TGCATCGGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196229

QY 661 CAGATGCCAAGCGTGCACCGCGGTGCCACCGCGGGGGTCCGACGCGCGTCCG 720
Db 196230 CAGATGCCAAGCGTGCACCGCGGTGCCACCGCGGGGGTCCGACGCGCGTCCG 196289

QY 721 GCGCCGCGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 196290 GCGCCGCGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 196349

QY 781 CCGGGGGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840

Db 196350 CCGGGGGGCGGAGAGCGGCGGAGCGCTGCCACCGAGCTCAACGGCGCGCTTGGGAGCCCC 196409

QY 841 GCGCGGCGCGGGCGCGGACACGACGCGCTGGACCTGGAGGAGAGCTCTCTTCCGAC 900

Db 196410 GCGCGGCGCGGGCGCGGACACGACGCGCTGGACCTGGAGGAGAGCTCTCTTCCGAC 196469

QY 901 CACGCCGAGCGGCTTCCAGGGCGCGGACGCCGAGACCGGAGCGGCTCCCGGGGCAAGCAAG 960

Db 196470 CACGCCGAGCGGCTTCCAGGGCGCGGACGCCGAGACCGGAGCGGCTCCCGGGGCAAGCAAG 196529

QY 961 GCCGAGCGAGCGAGGTGAACCGGGGCGGACGCTGCCGCGGCGGCGGCGGCGGCGGCGG 1020

Db 196530 GCCGAGCGAGCGAGGTGAACCGGGGCGGACGCTGCCGCGGCGGCGGCGGCGGCGGCGG 196589

QY 1021 GGGATCGGAGCGCGGCTGCGAGGGCGGGGAGGAGGCGGCTGCCAAGCGCGCTCG 1080

Db 196590 GGGATCGGAGCGCGGCTGCGAGGGCGGGGAGGAGGCGGCTGCCAAGCGCGCTCG 196649

QY 1081 CGTGGCGCGGGGCGGACGACCGGAGAGCGCTTACAGTTCGTGCTGCGGCGTGGTCAATC 1140

Db 196650 CGTGGCGCGGGGCGGACGACCGGAGAGCGCTTACAGTTCGTGCTGCGGCGTGGTCAATC 196709

QY 1141 GGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

Db 196710 GGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 196769

QY 1201 TGCTCCGTCGACGACGCTCTTCAAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

Db 196770 TGCTCCGTCGACGACGCTCTTCAAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 196829

QY 1261 TTGAACCGCGGCTATACACCATCTTCAACCGAGATTTCCGCGCGGCTTCAAGAGATC 1320

Db 196830 TTGAACCGCGGCTATACACCATCTTCAACCGAGATTTCCGCGCGGCTTCAAGAGATC 196889

QY 1321 CTCGTCGGGGGCGGAGGAGCGGATGCTG 1350

Db 196890 CTCGTCGGGGGCGGAGGAGCGGATGCTG 196919

RESULT 9
HUMADRA2R 3604 bp DNA linear PRI 30-OCT-1994
LOCUS Human alpha 2 adrenergic receptor gene, complete cds.
DEFINITION Human alpha 2 adrenergic receptor gene, complete cds.
ACCESSION M23533.1
VERSION M23533.1 GI:178195
KEYWORDS adrenergic receptor; alpha-2 adrenergic receptor.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3604)
AUTHORS Fraser, L.C.M., Arakawa, S., McCombie, W.R. and Venter, J.C.
TITLE Cloning, sequence analysis, and permanent expression of a human
alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylate
cyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)
PUBMED 89308571
COMMENT 2568356
Draft entry and computer-readable sequence for [1] kindly submitted
by W.R.McCombie, 30-MAR-1989.
FEATURES
source
1. 3604
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10q23-q25"
1578..1583
/bound_moiety="spl"
1707..1712
/note="glucocorticoid response element"
1723..1728
/note="GRE related sequence"



[illegible]



GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:30:36 ; Search time 725.473 Seconds
(without alignments)
915.286 Million cell updates/sec

Title: US-09-636-259C-1_COPY_730_770

Perfect score: 41

Sequence: 1 gggggcaccgagcgagcgcccgagcg 41

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_nam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41	100.0	453	14	BQ129312
C 2	41	100.0	492	14	BM967243
C 3	41	100.0	561	14	BM967248
C 4	25	61.0	235	9	AV250353
C 5	25	61.0	3689	11	AK014589
C 6	24.2	59.0	1350	14	BQ717347

7	24	58.5	763	12	BE905292
8	23.6	57.6	434	9	AI189117
9	23.6	57.6	606	9	AI935256
C 10	23.6	57.6	925	12	BG172901
C 11	23.4	57.1	463	14	BM800068
C 12	23.4	57.1	529	14	BM704323
C 13	23.4	57.1	606	14	BM671529
C 14	23.4	57.1	659	13	BI330755
C 15	23.4	57.1	793	13	BI952735
C 16	23	56.1	319	10	AM447119
C 17	23	56.1	389	13	BI915223
C 18	23	56.1	408	12	BE752287
C 19	23	56.1	420	12	BF600411
C 20	23	56.1	428	9	AI205341
C 21	23	56.1	451	12	BE753851
C 22	23	56.1	497	12	BF600543
C 23	23	56.1	516	13	BI848662
C 24	23	56.1	544	9	AI047807
C 25	23	56.1	552	13	BI976295
C 26	23	56.1	566	13	BI681538
C 27	23	56.1	737	12	BF315323
C 28	23	56.1	846	12	BG036904
C 29	23	56.1	876	12	BF314479
C 30	23	56.1	912	9	AL528396
C 31	23	56.1	915	12	BG030490
C 32	23	56.1	948	13	BI194887
C 33	23	56.1	955	14	BQ945746
C 34	23	56.1	967	14	BQ429819
C 35	23	56.1	1068	13	BI198127
C 36	23	56.1	1568	14	BQ222060
C 37	23	56.1	2101	11	AV106418
C 38	22.6	55.1	259	13	BI243119
C 39	22.6	55.1	237	13	BI482295
C 40	22.6	55.1	333	17	B71333
C 41	22.6	55.1	393	13	BI589545
C 42	22.6	55.1	438	13	BI353926
C 43	22.6	55.1	448	13	BI241551
C 44	22.6	55.1	457	13	BI578058
C 45	22.6	55.1	467	13	BI584252

ALIGNMENTS

RESULT 1
BQ129312/c
LOCUS
DEFINITION
i134d05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
CDNA clone IMAGE:6136736 5' similar to SW:A2AA_HUMAN P08913
ALPHA-2A ADRENERGIC RECEPTOR ; mRNA sequence.
BQ129312
VERSION
BQ129312.1 GI:20203223
KEYWORDS
EST.
SOURCE
HUMAN.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, J., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: i134d05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812

Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through LLNL; please contact the IMAGE
 consortium (info@image.llnl.gov) for further information
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco.

FEATURES

source
 1. .453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6136736"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
 Site 2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaudo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an Ecot of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 41 a 189 c 164 g 59 t

Query Match 100.0%; Score 41; DB 14; Length 453;

Best Local Similarity 100.0%; Pred. No. 0.00055;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGAGCGAGCCCAACGGTCTGGGCCCCGAGCG 41

DB 441 GGGGGCAGCGAGCGAGCCCAACGGTCTGGGCCCCGAGCG 401

RESULT 2

BM967243/c
 LOCUS BM967243
 DEFINITION iJ32c09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:6136336 5' similar to SW:A2AA_HUMAN P08913
 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION BM967243.1 GI:19561038

VERSION BM967243

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 492)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
 M., Gibbons M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
 Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Other ESTs: iJ32c09.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu)

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gibco

High quality sequence stop: 455.

FEATURES

source
 1. .492
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6136336"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
 Site 2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaudo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an Ecot of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 44 a 202 c 182 g 64 t

Query Match 100.0%; Score 41; DB 14; Length 492;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCAGCGAGCGAGCCCAACGGTCTGGGCCCCGAGCG 41

DB 441 GGGGGCAGCGAGCGAGCCCAACGGTCTGGGCCCCGAGCG 401

RESULT 3

BM967248/c
 LOCUS BM967248
 DEFINITION iJ32d04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:6136374 5' similar to SW:A2AA_HUMAN P08913
 ALPHA-2A ADRENERGIC RECEPTOR ;, mRNA sequence.

ACCESSION BM967248.1 GI:19561047

VERSION BM967248

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 561)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
 M., Gibbons M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
 Jackson,Y. and Bowers,Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Other ESTs: iJ32d04.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

IMAGE:6196278 5', mRNA sequence.
 B0717347
 VERSION B0717347.1 GI:21856244
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1350)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM13604 row: h column: 07
 High quality sequence stop: 200.
 BASE COUNT 213 a 379 c 521 g 235 t 2 others
 ORIGIN
 Query Match 59.0%; Score 24.2; DB 14; Length 1350;
 Best Local Similarity 78.4%; Pred. No. 2.8e-02;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 4 GGACCGCGCGCGCGCCACGCTCTGGCCCGCAGC 40
 Db 1056 GCCACCGCGCGCGCGCCACGCTCTGTGCCCGCCAGC 1020
 RESULT 7
 BE905292 763 bp mRNA linear EST 20-OCT-2000
 LOCUS BE905292
 DEFINITION mRNA sequence.
 ACCESSION BE905292
 VERSION BE905292.1 GI:10398430
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 763)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

IMAGE:6196278 5', mRNA sequence.
 B0717347
 VERSION B0717347.1 GI:21856244
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1350)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM13604 row: h column: 07
 High quality sequence stop: 200.
 BASE COUNT 213 a 379 c 521 g 235 t 2 others
 ORIGIN
 Query Match 59.0%; Score 24.2; DB 14; Length 1350;
 Best Local Similarity 78.4%; Pred. No. 2.8e-02;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 4 GGACCGCGCGCGCGCCACGCTCTGGCCCGCAGC 40
 Db 1056 GCCACCGCGCGCGCGCCACGCTCTGTGCCCGCCAGC 1020
 RESULT 7
 BE905292 763 bp mRNA linear EST 20-OCT-2000
 LOCUS BE905292
 DEFINITION mRNA sequence.
 ACCESSION BE905292
 VERSION BE905292.1 GI:10398430
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 763)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

IMAGE:6196278 5', mRNA sequence.
 B0717347
 VERSION B0717347.1 GI:21856244
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1350)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM13604 row: h column: 07
 High quality sequence stop: 200.
 BASE COUNT 213 a 379 c 521 g 235 t 2 others
 ORIGIN
 Query Match 59.0%; Score 24.2; DB 14; Length 1350;
 Best Local Similarity 78.4%; Pred. No. 2.8e-02;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 4 GGACCGCGCGCGCGCCACGCTCTGGCCCGCAGC 40
 Db 1056 GCCACCGCGCGCGCGCCACGCTCTGTGCCCGCCAGC 1020
 RESULT 7
 BE905292 763 bp mRNA linear EST 20-OCT-2000
 LOCUS BE905292
 DEFINITION mRNA sequence.
 ACCESSION BE905292
 VERSION BE905292.1 GI:10398430
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 763)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

IMAGE:6196278 5', mRNA sequence.
 B0717347
 VERSION B0717347.1 GI:21856244
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1350)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM13604 row: h column: 07
 High quality sequence stop: 200.
 BASE COUNT 213 a 379 c 521 g 235 t 2 others
 ORIGIN
 Query Match 59.0%; Score 24.2; DB 14; Length 1350;
 Best Local Similarity 78.4%; Pred. No. 2.8e-02;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 4 GGACCGCGCGCGCGCCACGCTCTGGCCCGCAGC 40
 Db 1056 GCCACCGCGCGCGCGCCACGCTCTGTGCCCGCCAGC 1020
 RESULT 7
 BE905292 763 bp mRNA linear EST 20-OCT-2000
 LOCUS BE905292
 DEFINITION mRNA sequence.
 ACCESSION BE905292
 VERSION BE905292.1 GI:10398430
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 763)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

IMAGE:6196278 5', mRNA sequence.
 B0717347
 VERSION B0717347.1 GI:21856244
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1350)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM13604 row: h column: 07
 High quality sequence stop: 200.
 BASE COUNT 213 a 379 c 521 g 235 t 2 others
 ORIGIN
 Query Match 59.0%; Score 24.2; DB 14; Length 1350;
 Best Local Similarity 78.4%; Pred. No. 2.8e-02;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 4 GGACCGCGCGCGCGCCACGCTCTGGCCCGCAGC 40
 Db 1056 GCCACCGCGCGCGCGCCACGCTCTGTGCCCGCCAGC 1020
 RESULT 7
 BE905292 763 bp mRNA linear EST 20-OCT-2000
 LOCUS BE905292
 DEFINITION mRNA sequence.
 ACCESSION BE905292
 VERSION BE905292.1 GI:10398430
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 763)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

went through one round of normalization. Library constructed by M. Fatima Bonaldo."

```

BASE COUNT      83 a      93 c      146 g      112 t
ORIGIN

Query Match      57.6%; Score 23.6; DB 9; Length 434;
Best Local Similarity 76.3%; Pred. No. 3.6e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY  4  GGCACCGCGCCGAGCCCAACGGTCTGGGCCCCGAGCG 41
|||||
Db  426 GGCACCGCGCCGCGCCCAACGGTCTGGGCCCCGAGCG 389
|||||

RESULT 9
AI935256      606 bp      mRNA      linear      EST 08-MAR-2000
LOCUS      wp16a07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464980 3',
DEFINITION      mRNA sequence.
ACCESSION      AI935256
VERSION      AI935256.1 GI:5674126
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 606)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 652 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 390.

FEATURES
source
1..606
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:2464980"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT773 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT      113 a      219 c      197 g      77 t
ORIGIN

Query Match      57.6%; Score 23.6; DB 9; Length 606;
Best Local Similarity 76.3%; Pred. No. 3.9e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY  3  GGCACCGAGCGCAGCGCCCAACGGTCTGGGCCCCGAGC 40
|||||

```

Db 146 GAGCGCGCCCGCAGGGCCCGAGGCTGTGGCCCCCGAGC 183

```

RESULT 10
BG172901/c
LOCUS      602337361F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4460270 5',
DEFINITION      mRNA sequence.
ACCESSION      BG172901
VERSION      BG172901.1 GI:12679617
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 925)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10261 row: j column: 15
High quality sequence stop: 652.

FEATURES
source
1..925
/organism="Mus musculus"
/db xref="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:4460270"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT      180 a      271 c      274 g      200 t
ORIGIN

Query Match      57.6%; Score 23.6; DB 12; Length 925;
Best Local Similarity 76.3%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY  4  GGCACCGAGCGCAGCGCCCAACGGTCTGGGCCCCGAGCG 41
|||||
Db  862 GGCACCGCGCGCGGCCCAACCTCAGGGCCCCCAAGAG 825
|||||

RESULT 11
BM800068/c
LOCUS      AGENCOURT_6415956 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531068
DEFINITION      5', mRNA sequence.
ACCESSION      BM800068
VERSION      BM800068.1 GI:19116891
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 463)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12212 row: c column: 05
 High quality sequence stop: 462.
 Location/Qualifiers
 1. .463
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5531068"
 /clone_lib="NIH MGC 71"
 /tissue_type="lcnomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb."
 90 a 160 c 130 g 83 t

FEATURES

source

BASE COUNT 90 a 160 c 130 g 83 t

ORIGIN

Query Match 57.1%; Score 23.4; DB 14; Length 463;
 Best Local Similarity 73.2%; Pred. No. 4.3e+02;
 Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGCAGGCGCCACGCTCTGGGCCCGCAGCG 41
 |||||
 Db 358 GGGGGCACCAGCGCAGGCGCCACGCTCTGGGCCCGCAGCGG 318

RESULT 12

BM704323/c

LOCUS BM704323 529 bp mRNA linear EST 28-FEB-2002
 DEFINITION UI-E-CK1-afj-j-22-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone
 UI-E-CK1-afj-j-22-0-UI 5', mRNA sequence.

ACCESSION BM704323.1 GI:19017581

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 529)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1. .529

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-CK1-afj-j-22-0-UI"

/clone_lib="UI-E-CK1"

/tissue_type="Retina Foveal and Macular"

/dev_stage="adult"

FEATURES

source

1. .606

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-CK1-afj-j-22-0-UI"

/clone_lib="UI-E-CK1"

/tissue_type="Retina Foveal and Macular"

/dev_stage="adult"

/lab host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

/lab host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
 83 a 173 c 161 g 111 t 1 others

Query Match 57.1%; Score 23.4; DB 14; Length 529;

Best Local Similarity 73.2%; Pred. No. 4.4e+02;

Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGCAGGCGCCACGCTCTGGGCCCGCAGCG 41
 |||||
 Db 288 GGGGGCACCAGCGCAGGCGCCACGCTCTGGGCCCGCAGCGG 248

RESULT 13

BM671529

LOCUS

DEFINITION UI-E-CK1-afj-j-22-0-UI.s2 UI-E-CK1 Homo sapiens cDNA clone

UI-E-CK1-afj-j-22-0-UI 3', mRNA sequence.

ACCESSION BM671529.1 GI:18981427

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 606)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com).

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. .606

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-CK1-afj-j-22-0-UI"

/clone_lib="UI-E-CK1"

/tissue_type="Retina Foveal and Macular"

/dev_stage="adult"

UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is GRCC. this library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG LIB=UI-E-CK1
TAG_SEQ=Foveal and Macular Retina
TAG_SEQ=GTCC

BASE COUNT 138 a 173 c 189 g 104 t 2 others

ORIGIN

Query Match 57.1%; Score 23.4; DB 14; Length 606;
Best Local Similarity 73.2%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGCAGGCCAACAGGCTCTGGCCCCGAGCG 41
Db 325 GGGGGCACCAGCGCAGGCCAACAGGCTCTGGCCCCGAGCG 365

RESULT 14

BI330755

LOCUS

DEFINITION 602982420F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5135261 5', mRNA linear EST 30-JUL-2001

ACCESSION BI330755

VERSION BI330755.1 GI:15015412

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1. (bases 1 to 659)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM1132 row: g column: 06

High quality sequence stop: 655.

FEATURES

source

1. 659

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5135261"

/clone_lib="NCI CGAP Li9"

/lab_host="DH10B (TI phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 148 a 153 c 191 g 167 t

ORIGIN

Query Match 57.1%; Score 23.4; DB 13; Length 659;

Best Local Similarity 73.2%; Pred. No. 4.6e+02;

Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGGGCACCAGCGCAGGCCAACAGGCTCTGGCCCCGAGCG 41

Db 387 GGGGGCACCAGCGCAGGCCAACAGGCTCTGGCCCCGAGCG 427

RESULT 15

BI952735/c

LOCUS

DEFINITION 793 bp mRNA linear EST 19-OCT-2001
HVCdNA0014 (Blumeria infected) Hordeum vulgare cDNA clone
HVSME00007J12f, mRNA sequence.

ACCESSION BI952735

VERSION BI952735.1 GI:16296792

KEYWORDS EST.

SOURCE Hordeum vulgare.

ORGANISM Hordeum vulgare

REFERENCE 1. (bases 1 to 793)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
; Triticeae; Hordeum.

AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons,
J., Oates, R. and Main, D.

TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
cDNA library

JOURNAL Unpublished (2001)

COMMENT

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 198

Seq primer: AATTACCTCACTTAAGGG

High quality sequence start: 22

High quality sequence stop: 590.

Location/Qualifiers

1. 793

/organism="Hordeum vulgare"

/cultivar="Morex"

/db_xref="taxon:4513"

/clone="HVSME00007J12f"

/clone_lib="Hordeum vulgare green seedling EST library

HVCdNA0014 (Blumeria infected)"

/tissue_type="green seedling leaf"

/lab_host="TJCl21"

/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; Morex (mla) plants were greenhouse grown in the R

Wise lab at Iowa State University, Ames, IA; 7 day old

green seedlings were infected with isolate 5874 of

Blumeria graminis f. sp. hordei, and leaves were harvested

24, 48 and 72 hr post-inoculation and snap frozen (Wise).

In the TJ Close lab at the University of California,

Riverside, total RNA was prepared from each sample pool,

equal quantities of all three RNA pools were combined,

poly(A) RNA was purified from the mixture, one primary

unamplified cDNA library was made, and 1 million pfu were

in vivo excised to give pBluescript SK(-) cDNA phagemids

(Chin). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,

Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI

(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).

The sequence has been trimmed to remove vector sequence

and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order

this clone see http://www.genome.clemson.edu/orders Also

see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT 180 a 240 c 229 g 144 t

ORIGIN

Query Match 57.1%; Score 23.4; DB 13; Length 793;
Best Local Similarity 73.2%; Pred. No. 4.7e+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGGCACCAGCGAGCGCCCAACGGTCTGGGCCCCGAGCG 41

DB 743 GGGGGTTCGCGCCCCCAGCCTAAGGTCTGGGCCCCGAGTG 703

Search completed: March 11, 2003, 07:38:58
Job time : 733.473 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: March 10, 2003, 18:28:11 ; Search time 20004.5 Seconds
(without alignments)
1964.002 Million cell updates/sec

Title: US-09-636-259C-1
Perfect score: 1350
Sequence: 1 atgggctccctgcagccgga.....gggacaggaagcgatcgtg 1350

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank :
1: gb_ba :
2: gb_hg :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sts :
12: gb_sy :
13: gb_un :
14: gb_vi :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
19: em_mu :
20: em_om :
21: em_or :
22: em_ov :
23: em_pat :
24: em_ph :
25: em_pl :
26: em_ro :
27: em_sts :
28: em_un :
29: em_vi :
30: em_hg_hum :
31: em_hg_inv :
32: em_hg_other :
33: em_hg_mus :
34: em_hg_pln :
35: em_hg_rod :
36: em_hg_mam :
37: em_hg_vrt :
38: em_sv :
39: em_hggo_hum :
40: em_hggo_mus :
41: em_hggo_other :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1350	100.0	1350	6	AX350512	Sequence
2	1350	100.0	1353	9	AF281308	Homo sapi
3	1350	100.0	1941	9	AF262016	Homo sapi
4	1350	100.0	3612	9	AY032736	Homo sapi
5	1350	100.0	3653	9	AF284095	Homo sapi
6	1350	100.0	204908	9	AL158163	Human DNA
7	1348.4	99.9	1350	6	AX350513	Sequence
8	1348.4	99.9	1353	9	AF316894	Homo sapi
9	1327	98.3	3604	9	HUMADRA2R	Homo sapi
10	1319	97.7	1521	9	HUMADRA	Human place
11	1150	85.2	1728	4	PIGA2AR	Porcine alp
12	1133.8	84.0	2291	10	CPU25722	Cavia porce
13	1106.8	82.0	1552	10	RRU79031	Rattus norv
14	1095.6	81.2	1380	10	RATRG20	Rat alpha-2
15	1095	81.1	2923	4	BTU79030	Bos taurus
16	1084.4	80.3	1454	10	MUSALP2ADB	Mouse alpha
17	1084.4	80.3	204317	2	AC113491	Mus muscu
18	917	67.9	7353	6	AX344975	Sequence
19	917	67.9	7353	6	AX348496	Sequence
20	838	62.1	7353	6	AX344974	Sequence
21	838	62.1	7353	6	AX348495	Sequence
22	529.6	39.2	1386	6	AX350528	Sequence
23	529	39.2	1491	9	HUMADRA2C	Human kidne
24	529	39.2	4850	9	HSU72648	Homo sapien
25	526.4	39.0	1389	9	AF280399	Homo sapi
26	518.8	38.4	1374	6	AX350530	Sequence
27	516.2	38.2	1995	10	CPU25724	Cavia porce
28	515.6	38.2	1377	9	AF280400	Homo sapi
29	514	38.1	1382	6	E07358	GDNA encodi
30	514	38.1	1382	9	HUMA2C1IA	Human alpha
31	506.8	37.5	3461	5	TRU345040	Takifugu
32	462.8	34.3	1503	10	MUSALP2ADA	Mouse alpha
33	462.8	34.3	1745	10	RATA2AR	Rattus norv
34	462	34.2	1380	10	RATRG10	Rat alpha-2
35	460.4	34.1	2991	10	RNA2C4	R. norvegic
36	460.4	34.1	5221	10	MUSADRA	Mus musculu
37	458.8	34.0	1704	10	RATA2BADR	Rat alpha-2
38	446	33.0	22842	9	AC092603	Homo sapi
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ALIGNMENTS

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LOCUS AX350512 1350 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 24 from Patent WO0179561.
ACCESSION AX350512
VERSION AX350512.1 GI:18616107
KEYWORDS human.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Liggett S.B. and Small K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 24 25-OCT-2001;

Query Match		100.0%	Score 1350;	DB 9;	Length 1353;
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Best Local Similarity 99.9%; Pred. No. 3.6e-159;
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RESULT 9
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DEFINITION Human alpha 2 adrenergic receptor gene, complete cds.
ACCESSION M23533
VERSION M23533.1 GI:178195
KEYWORDS adrenergic receptor; alpha-2 adrenergic receptor.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3604)
AUTHORS Fraser, C.M., Arakawa, S., McCombie, W.R. and Venter, J.C.
TITLE Cloning, sequence analysis, and permanent expression of a human alpha 2-adrenergic receptor in Chinese hamster ovary cells.
Evidence for independent pathways of receptor coupling to adenylylate cyclase attenuation and activation
J. Biol. Chem. 264 (20), 11754-11761 (1989)
JOURNAL 89308571
MEDLINE 2568356
PUBMED
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by W.R. McCombie, 30-MAR-1989.
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DEFINITION
ACCESSION M18415
VERSION M18415.1 GI:178191
KEYWORDS alpha-2-adrenergic receptor; alpha-adrenergic receptor.
SOURCE Human (lambda-EMBL 3 library) DNA.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bukayvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Kobilka,B.K., Matsui,H., Kobilka,T.S., Yang-Feng,T.L., Francke,U.,
Caron,M.G., Lefkowitz,R.J. and Regan,J.W.
Cloning, sequencing, and expression of the gene coding for the
human platelet alpha 2-adrenergic receptor
JOURNAL Science 238 (4827), 650-656 (1987)
MEDLINE 88042789
PUBMED 2823383
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2003, 12:29:07 : Search time 4002.27 Seconds
(without alignments)
9816.632 Million cell updates/sec

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Perfect score: 1350
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
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- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1350	100.0	1350	6	AX350513	Sequence
2	1350	100.0	1353	9	AF316894	Homo sapi
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16	1082.8	80.2	1454	10	MUSALP2ADB	Bos taurus
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36	462	34.2	5221	10	MUSADRA	R. norvegic
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Sequence 25 from Patent WO0179561.
ACCESSION AX350513
VERSION AX350513.1
KEYWORDS GI:18616108
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 25 25-OCT-2001;

linear PAT 06-FEB-2002


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LOCUS Homo sapiens alpha 2A adrenergic receptor (ADRA2A) gene, complete
DEFINITION
ACCESSION AF281308
VERSION AF281308.1 GI:9652209
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Brown,K.M. and Liggett,S.B.
TITLE An asn to lys polymorphism in the third intracellular loop of the
human alpha 2A-adrenergic receptor imparts enhanced
agonist-promoted Gi coupling
J. Biol. Chem. 275 (49), 38518-38523 (2000)
MEDLINE 20556293
PUBMED 10948191
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REFERENCE
AUTHORS Small,K.M., Forbes,S.L., Bridges,K.M. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave., Cincinnati, OH 45267, USA
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